REMARKS

In the Office Action, Claims 25 to 36 were objected to as allegedly being substantial duplicates of Claims 1 to 12. The objection is respectfully traversed.

Applicant notes that the objection is flawed in that MPEP 706.03(k) calls for an objection regarding duplicate claims to be entered *only* when other claims of which the alleged duplicate claims read-on have been allowed. In the present case, the Office Action specifically states at page 6 that "no claims are allowed." Therefore, entry of an objection at this time is clearly improper.

Nonetheless, it is respectfully submitted that Applicant is merely plural claiming the present invention, which has been held by the courts to be acceptable practice. (See MPEP 706.03(k), stating that "court decisions have confirmed applicant's right to restate (i.e., by plural claiming) the invention in a reasonable number of ways," and "a mere difference in scope between claims has been held to be enough.) In this regard, the two sets of claims vary in scope at least in that one set (Claims 1 to 12) is directed to a method of interpreting data, which may be performed in any number of ways, while the other set (Claims 25 to 36) is directed to a computer program executable by a computer to interpret the data. Thus, while the claims may contain some similar phraseology, they do nonetheless vary in the scope. Therefore, it is submitted that the invention is merely being plural claimed and the objection is believed to be improper. Accordingly, withdrawal of the duplicate claim objection for Claims 25 to 36 is respectfully requested.

Claims 1 to 3, 6, 13 to 15, 18, 25 to 27, 30, 37 to 39 and 42 were rejected under 35 U.S.C. § 102(b) over an article to Ewing, et al., entitled "Base-Calling of Automated Sequencer Traces Using *Phred.* I. Accuracy Assessment" (hereinafter referred

to as "Ewing"). In addition, Claims 5 to 12, 17 to 24, 29 to 36 and 41 to 48 were rejected under 35 U.S.C. § 103(a) over Ewing in view of an article to Youssef, entitled "Lossy Compression-Transforms" and further in view of an article to Curram et al., entitled "Neural Networks, Decision Tree Induction and Discriminant Analysis: an Empirical Comparison". It is noted that, although the Office Action Summary indicates that all of Claims 1 to 48 have been rejected, the Detailed Action portion of the Office Action does not include any art based rejections of Claims 4, 16, 28 and 40. Applicant's undersigned attorney contacted the Examiner on June 26, 2003 and requested a status of these claims, but to date, no status has been provided by the Examiner. Therefore, since there is no express indication of allowability in the Office Action, in accordance with MPEP 707.07(d), Applicant will treat Claims 4, 16, 28 and 40 as having been rejected for the same reasons as their base claims. However, clarification of the status of Claims 4, 16, 28 and 40 is respectfully requested. As for the rejections, they are respectfully traversed and the Examiner is requested to reconsider and the withdraw the rejections in light of the following comments.

The present invention concerns interpretation of nucleic acid data. According to the invention, the nucleic acid data is first obtained in a spatial domain. For example, a gel electrophoresis process may be performed on nucleic acid material to obtain an image that is then converted into a machine-readable format of the nucleic acid data in the spatial domain. The invention, unlike conventional methods, transforms the nucleic acid data obtained in the spatial domain to a frequency domain. That is, the machine-readable form of the spatial domain nucleic acid data is subjected to a transformation process using, for example, Hadamard transforms, Fourier transforms, Wavelet transforms,

etc., such that the nucleic acid data itself is transformed from the spatial domain to the frequency domain. As described in the specification, the transformation of the nucleic acid data from the spatial domain to the frequency domain minimizes "within-class" variability and maximizes "between-class" variability of features of interest, such as allele patterns. Once the nucleic acid data has been transformed to the frequency domain, a data mining process is then performed on the transformed (i.e., frequency domain) nucleic acid data to obtain sequence data. As a result, the transformation to the frequency domain removes or reduces redundancies in the pattern recognition process, and additionally, the amount of data subjected to the data mining process is reduced so as to increase the efficiency of the pattern recognition process.

Referring specifically to the claims, independent Claim 1 is a method of interpreting data obtained from the analysis of nucleic acids, comprising the steps of obtaining the nucleic acid data in a spatial domain, transforming the nucleic acid data from the spatial domain to a frequency domain, and obtaining sequence data of the transformed data by executing a data mining process on the transformed nucleic acid data.

Independent Claims 13, 25 and 37 are apparatus, computer-executable process steps, and computer-readable medium claims, respectively, that substantially correspond to Claim 1.

The applied art, alone or in any permissible combination, is not seen to disclose or to suggest the features of Claims 1, 13, 25 and 37, and in particular is not seen to disclose or to suggest at least the feature of transforming nucleic acid data from a spatial domain to a frequency domain. As a result, the applied art also is not seen to disclose or to suggest at least the feature of executing a data mining process on the transformed

(frequency domain) nucleic acid data to obtain sequence data.

Ewing is seen to disclose a base-calling program (*Phred*) that aims to improve the accuracy of detecting the location of peaks. The *Phred* program performs the following: 1) inputting a chromatogram file, 2) normalizing the data of the chromatogram to form a skyline projection, 3) performing peak prediction to predict the ideal location of base peaks, 4) locating actual observed peaks, 5) matching the observed peaks with the predicted peaks, and 6) finding missed peaks. Applicant submits that steps 1) and 2) of Ewing may be seen to respectively correspond to the obtaining nucleic acid data in the spatial domain step of, for example, Claim 1, and the normalization process of, for example, Claim 3. However, the remaining steps of Ewing are significantly different from the frequency domain transformation and data mining steps of Claims 1, 13, 25 and 37.

Ewing's step 3) performs peak prediction by examining trace arrays to detect the location of maximum values. The trace is also scanned to find regions of uniform spacing, with the spacing being compared with the detected maximum values to determine period values. The maximum values, spacing and period values are then used in simple Fourier methods to form a sine wave that represents a predicted peak pattern. The sine wave is then used to determine the predicted peaks by determining the maximum values that are closest to the center of each region of the sine wave. Thus, the peak prediction process of Ewing merely uses Fourier methods to generate a sine wave, but Fourier methods are not used to transform the nucleic acid data to the frequency domain.

In this regard, the nucleic acid data itself of Ewing is not transformed in the peak prediction process, but rather, the maximum values and spacing data are merely used to seed the Fourier methods for generating the sine wave. That is, in Ewing's step 3), some

values are obtained from the spatial domain nucleic acid data to seed the peak prediction process, but the nucleic acid data itself remains in its original spatial domain form. As evidence of this, in Ewing's step 4), the spatial domain nucleic acid data is analyzed, utilizing conventional techniques, to obtain observed peaks. The purpose of the peak prediction process is to check the accuracy of the observed peaks of Ewing's step 4) by comparing (Ewing's step 5) the predicted peaks with the actual observed peaks. Thus, the nucleic acid data of Ewing is not transformed to the frequency domain, but remains in the spatial domain. Accordingly, since Ewing does not transform the nucleic acid data from the spatial domain to the frequency domain, Ewing also cannot perform a data mining process on the transformed nucleic acid data to obtain sequence data as claimed in the present invention. In view of the foregoing, independent Claims 1, 13, 25 and 37 are not believed to be anticipated by Ewing.

Youssef and Curram are not seen to add anything that, when combined with Ewing, would have overcame Ewing's deficiencies or that would have rendered the present invention obvious. Youssef is merely seen to disclose the use of various data compression techniques to transform data. Some techniques disclosed in Youssef include Fourier transforms, DCT (Discrete Cosine Transforms), Hadamard transforms and Wavelet transforms. It is hereby submitted that the use of any one or more of the foregoing methods for transforming data in general is not new, nor is Applicant claiming that he has invented a new transformation method. However, it has not heretofore been known to use any type of transform technique in interpreting data obtained by analysis of nucleic acid data to transform the nucleic acid data obtained in a spatial domain to a frequency domain as

claimed in the present invention. Youssef itself fails to mention anything with regard to transforming nucleic acid data from a spatial domain to a frequency domain.

Moreover, it is submitted that the present invention would not have been obvious from any permissible combination of the applied art. Assuming arguendo that Ewing and Youssef could have been combined, such a combination still would not have rendered the present invention obvious. In this regard, neither Ewing or Youssef disclose or suggest transforming the nucleic acid data obtained in the spatial domain to the frequency domain. As stated above, Ewing's nucleic acid data is not transformed, but remains in the spatial domain. Youssef, on the otherhand, makes no mention whatsoever regarding nucleic acid data, muchless applying any of the transformations disclosed therein to nucleic acid data. Thus, a combination of Ewing and Youssef would not have resulted in the present invention.

Additionally, it is submitted that, at best, a combination of Ewing and Youssef would have resulted in any one or more of the transforms disclosed in Yousseff being applied to the peak prediction process of Ewing. The use of such other transforms would merely have provided for generating a peak prediction curve in a different manner than using the Fourier methods disclosed in Ewing. However, the nucleic acid data of Ewing still would not have been transformed since nothing in either Ewing or Yousseff discloses or suggests transforming the nucleic acid data from the spatial domain to the frequency domain. Only Applicant's specification provides the suggestion to perform such a process and therefore, application of Youssef's transformations to transform the nucleic acid data of Ewing would be impermissible hindsight. Accordingly, the present invention would not have been obvious from any permissible combination of Ewing and Youssef.

Curram has been studied but is not seen to add anything to overcome the deficiencies of Ewing and Youssef. Curram is merely seen to disclose the use of neural networks in data analysis. However, like Ewing and Youssef, Curram fails to disclose or to suggest anything with regard to transforming nucleic acid data from a spatial domain to the frequency domain, and performing a data mining process on the transformed data to obtain sequence data.

In view of the foregoing deficiencies of the applied art, all of Claims 1 to 48 are believed to be allowable.

As a formal matter, Applicant notes that the Patent Office has not yet provided an indication whether the Petition for acceptance of color photographs, which was filed on December 21, 2001, has been granted. Therefore, clarification of the status of the Petition is respectfully requested.

No other matters having been raised, the entire application is believed to be in condition for allowance and such action is respectfully requested at the Examiner's earliest convenience.

Applicant's undersigned attorney may be reached in our Costa Mesa, California office at (714) 540-8700. All correspondence should continue to be directed to our below-listed address.

Respectfully submitted,

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